

413

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Scientific and Technical Information Center

SEARCH REQUEST FORM

Requester's Full Name: DAVID GUZO Examiner #: 70677 Date: 7/10/06
Art Unit: 1636 Phone Number: 2-0767 Serial Number: 10/765,456
Location (Bldg/Room#): Room 2A79 (Mailbox #): 2C70 Results Format Preferred (circle): PAPER DISK

To ensure an efficient and quality search, please attach a copy of the cover sheet, claims, and abstract or fill out the following:

Title of Invention: _____

Inventors (please provide full names): _____

Earliest Priority Date: _____

Search Topic: _____
Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc., if known.

For Sequence Searches Only Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.

*Please run a regular plus interference sequence
search on SEQ ID NO: 1 and 3.
rev 1 - 521AA
rev 3 - 1584NA*

T. Banks

RECEIVED
JUL 10 2006
STIC/CHEM. DIVISION
(STIC)

GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: July 11, 2006, 08:30:11 ; Search time 41 Seconds
(without alignments)
1236.737 Million cell updates/sec

Title: US-10-765-456-1
Perfect score: 2790
Sequence: 1 MNOISKNDSDLVLDQEMGQK.....YWEIMQFHNKROOLRAIIE 527

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 9621673 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	244.5	8.8	710	2 T50469	hypothetical prote
2	244.5	8.8	710	2 A25657	hypothetical prote
3	244.5	8.8	720	2 T50475	hypothetical prote
4	213	7.6	470	2 E97331	reverse transcript
5	205.5	7.4	418	2 H83677	transposase (11) B
6	204.5	7.3	418	2 G83654	transposase (11) B
7	178.5	6.4	599	2 S77648	transposase (11) B
8	171.5	6.1	453	2 A95946	transposase (11) B
9	166.5	6.0	790	2 E48327	COI intron A prote
10	163.5	5.9	392	2 G96004	probable reverse t
11	161	5.8	574	2 T90245	reverse transcript
12	157	5.6	788	2 B48327	reverse transcript
13	156.5	5.6	318	2 S58503	reverse transcript
14	155	5.5	602	2 G59091	hypothetical prote
15	154	5.5	461	2 G59093	hypothetical prote
16	154	5.5	668	2 A91989	retrovirus-related
17	154	5.5	1260	4 GNLRL1	retrovirus-related
18	153	5.5	368	2 S01651	probable RNA-direc
19	151	5.4	633	2 T131160	maturase-related p
20	148.5	5.3	1084	2 T131173	RNA-directed DNA p
21	146.5	5.3	608	2 S05341	probable reverse t
22	146	5.2	308	2 S58544	reverse transcript
23	144	5.2	785	2 S63652	reverse transcript
24	141	5.1	834	1 GAB131	hypothetical prote
25	141	5.1	834	2 S78642	gene cox1 intron 1
26	138.5	5.0	416	2 S50828	hypothetical prote
27	137	4.9	1352	2 G84473	hypothetical prote
28	136	4.9	330	2 E98119	transposase, uncha
29	136	4.9	860	2 S55543	RNA-directed DNA p

30	134.5	4.8	376	2 B64751	yKc protein - Esc
31	134.5	4.8	546	2 T11217	reverse transcript
32	133	4.8	571	2 T31170	maturase-related p
33	132.5	4.7	544	2 T11216	reverse transcript
34	131	4.7	1259	4 GNMH1	retrovirus-related
35	131	4.7	1275	2 S65824	reverse transcript
36	130	4.7	908	2 S07649	gene co1 intron 1
37	127.5	4.6	1045	2 S23570	pol polyprotein ho
38	127	4.6	1280	2 B34087	hypothetical prote
39	124.5	4.5	502	2 S26004	18S rRNA intron 1
40	124.5	4.5	600	2 AE2570	hypothetical prote
41	124.5	4.5	1226	2 H64479	hypothetical prote
42	123.5	4.4	1258	2 T14853	protoporphylin IX
43	120.5	4.4	827	2 S25949	reverse transcript
44	120.5	4.3	1224	2 S25952	gene cox1 intron
45	120.5	4.3	2517	2 S58380	probable RNA-direc

ALIGNMENTS

RESULT 1
T50469
hypothetical protein [imported] - Neurospora crassa mitochondrion plasmid Varkud
C:Species: mitochondrion Neurospora crassa
C:Date: 09-Jun-2000 #sequence_revision 09-Jun-2000 #text_change 09-Jul-2004
C:Accession: T50469
R:Akins, R.A.; Grant, D.M.; Stohl, L.L.; Bortoroff, D.A.; Nargang, F.E.; Lambowitz, A.M.
J. Mol. Biol. 204, 1-25, 1998
A:Title: Nucleotide sequence of the Varkud mitochondrial plasmid of Neurospora and synt
A:Reference number: Z25076; M01D:89110991; PMID:3216387
A:Accession: T50469
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-710 <AKI>
A:Cross-references: UNIPROT:Q35156; UNIPARC:UPI00000925A5; EMBL:X13801; NID:92941; PIDA
C:Genetics:
A:Genome: mitochondrion plasmid Varkud
A:Genetic code: SGC3
A:introns: 30/3
C:Keywords: mitochondrion

Query Match	Score	Length	ID	Description
Best local similarity	25.4%	244.5	DB 2	Length 710
Matches	95	Conservative	61	Mismatches 151; Indels 67; Gaps 13
1	MNOISKNDSDLVLDQEMGQKTFESERKSLSGMDYFKSLGSLGRPHFSRGIELREVKA	60		
10	VSYLEGHELSWLGWFGLEKRSNPOTGMLGWLNTG-----P	47		
61	NRYLAFQEOIRIVSAIEAGEIRKAVLWMLCKMKSRSYOILLFNVCCKWYRMSTARVEE	120		
48	NGFYKWMNLMGHARDGDAKEYRRLRSLSMK-NEAQVOAFNVCWCHWYADYFKHAK	106		
121	IIRGANKKMSWMDKLIHRYFYLLKQKXMRPIGAPNYESRMISKALTDML--SITKES	178		
107	LLEKREMEVLEOPVCIDYKRVYIPKANGKORPLGVPVPRVYILMMNVLLWYRIEOD	166		
179	RSAEHQGYMKKRGAMSAILECSKLEAGVAGYFEDLKSFFNTVPEPTFYFKLEE--VDK	236		
167	---NQHAYFPKRGVFTAWRLWPKL-DSQNIYFFDDKNFPFSDVLAFLKDKLMESGIPQD	222		
237	LTKLISNVIKGIEYRFE--LLPE-----SELNPKARKNTLB-----	272		
223	ISEYLVLRSLVVLSEDKIPEPHDVFENSDGTPNPVLPRDVOGRILKDPFVEILRR	282		
273	-----RTGVPGGSLSPLLSTWAL-EYVGRPENLINVADGIYFFKKNISKFTWIR	324		
283	RGFTDIATNGVPGASTSCGLATYVNVKELFKYDELIWYADGCI-LCRDPPSTPPSIE-	340		
325	MGRAGIEISPEKSG	338		
341	---EAGVQDEPAKSG	352		

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OM protein - protein search, using sw model

Run on: July 11, 2006, 08:26:50 ; Search time 300 Seconds

(without alignments)
1624.944 Million cell updates/sec

Title: US-10-765-456-1

Perfect score: 2790
Sequence: 1 MNOISKNDSDVLDQENKGRK.....YWEIMQFNLRQQLRAIIE 527

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database: 1: UniProt_7.2:*
2: UniProt_sprot:*
3: UniProt_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2790	100.0	527	2	Q9XNK5_FUSOX
2	2550	91.4	527	2	Q9XNK4_FUSOX
3	2052	73.5	397	2	Q21164_FUSOX
4	420	15.1	262	2	Q21165_FUSOX
5	315	11.3	605	2	Q9MEH5_TRIFA
6	270.5	9.7	294	2	Q9XMG3_EPTTY
7	245.5	8.8	710	2	Q595Q1_NEUIN
8	244.5	8.8	710	2	Q595Q0_NEUIN
9	244.5	8.8	710	2	Q7GEY3_NEUCR
10	244.5	8.8	720	2	Q35156_NEUIN
11	243.5	8.7	710	2	Q36578_NEUCR
12	227.5	8.2	439	2	Q3CZ44_STRAG
13	227.5	8.2	439	2	Q8E028_STRAS
14	220	7.9	482	2	Q3GDE8_PIRIM
15	219.5	7.9	433	2	Q2MLJ7_CLOBE
16	216.5	7.8	470	2	Q3CK71_THEET
17	214.5	7.7	470	2	Q3CJ27_THEET
18	214	7.7	462	2	Q3JP84_PSPHI
19	213.5	7.7	470	2	Q3CES5_THEET
20	213	7.6	470	2	Q3CGY6_THEET
21	213	7.6	470	2	Q97DG3_CLOAB
22	212	7.6	470	2	Q3CUR9_THEET
23	212	7.6	470	2	Q3CK48_THEET
24	211.5	7.6	468	2	Q8A412_BACTN
25	210.5	7.5	412	2	Q7STM9_9BACI
26	210	7.5	412	2	Q3CEU2_THEET
27	209	7.5	470	2	Q3CJ31_THEET
28	208.5	7.5	469	2	Q420Q7_DESHA
29	207	7.4	470	2	Q3CER4_THEET
30	207	7.4	470	2	Q3CG40_THEET
31	207	7.4	470	2	Q3CGH0_THEET

32	205.5	7.4	418	2	Q9KG88_BACHD	Q9KG88 bacillus ha
33	205.5	7.4	423	2	Q4UCS6_LACRE	Q4UCS6 lactobacilli
34	205.5	7.4	604	2	Q732Q3_BACCI	Q732Q3 bacillus ce
35	205	7.3	418	2	Q75TR9_BACHD	Q75TR9 bacillus ha
36	204.5	7.3	412	2	Q75TN1_BACAG	Q75TN1 bacillus ag
37	204.5	7.3	412	2	Q75TN5_BACCI	Q75TN5 bacillus ci
38	204.5	7.3	412	2	Q75TR5_BACCI	Q75TR5 bacillus fi
39	204.5	7.3	418	2	Q75TR8_BACHD	Q75TR8 bacillus ha
40	204.5	7.3	418	2	Q9JWR9_BACHD	Q9JWR9 bacillus ha
41	204	7.3	434	2	Q74AB9_GEOSL	Q74AB9 geobacter s
42	203.5	7.3	418	2	Q75TN8_9BACI	Q75TN8 bacillus ha
43	203.5	7.3	418	2	Q75TN2_BACCS	Q75TN2 bacillus cl
44	202.5	7.3	418	2	Q75TR2_BACHD	Q75TR2 bacillus ha
45	198.5	7.1	627	2	Q74PE0_BACCI	Q74PE0 bacillus ce

ALIGNMENTS

RESULT 1	ID	Q9XNK5_FUSOX	PRELIMINARY; PRT; 527 AA.
AC	Q9XNK5		
DT	01-NOV-1999		Integrated into UniProtKB/TrEMBL.
DT	01-NOV-1999		sequence version 1.
DT	07-FEB-2006		entry version 23.
DE	Reverse transcriptase.		
OS	Fusarium oxysporum f. sp. raphani.		
OG	Mitochondrion.		
OG	Plasmid pFOX2.		
OC	Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;		
OC	Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium;		
OC	Fusarium oxysporum complex.		
OX	NCBI_TaxID=96318;		
OX	[1]		
RP	NUCLEOTIDE SEQUENCE.		
RC	STRAIN=699;		
RA	MEDLINE=99417962; PubMed=10488338; DOI=10.1016/S1097-2765(00)80370-6;		
RA	Walther T.C.; Kennell J.C.;		
RT	"Linear mitochondrial plasmids of F. oxysporum are novel, telomere-		
RT	like retroelements."		
RL	Mol. Cell 4:229-238(1999).		
CC	-1- SIMILARITY: Contains 1 reverse transcriptase domain.		
CC	Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms		
CC	Distributed under the Creative Commons Attribution-NonCommercial License		
CC	EMBL, AF124843; AAD38503.1; -; Genomic DNA.		
DR	GO; GO:0005739; C:mitochondrion; IEA.		
DR	GO; GO:0003723; F:RNA binding; IEA.		
DR	GO; GO:0003644; F:RNA-directed DNA polymerase activity; IEA.		
DR	GO; GO:0006378; P:RNA-dependent DNA replication; IEA.		
DR	InterPro: IPR000477; RVTse.		
DR	Pfam: PF00078; RVT_1; 1.		
DR	PROSITE: PS50878; RT_POL; 1.		
KW	Mitochondrion; Plasmid; RNA-directed DNA polymerase.		
SQ	SEQUENCE 527 AA; 62085 MW; 605F5EA92B341C65 CRC64;		
Query Match	100.0%; Score 2790; DB 2; Length 527;		
Best Local Similarity	100.0%; Pred. No. 7e-188;		
Matches 527; Conservative	0; Mismatches 0; Indels 0; Gaps 0;		
QY	1	MNOISKNDSDVLDQENKGRKSLSGMDYFKSLGSLGRLLPHFSRGILREVKKA	60
DB	1	MNOISKNDSDVLDQENKGRKSLSGMDYFKSLGSLGRLLPHFSRGILREVKKA	60
QY	61	NRILAPOEQRIVSAIDAGIRKAVLYWLCIMKYSRSYQILLFNRVCKGWYRWSTARVEE	120
DB	61	NRILAPOEQRIVSAIDAGIRKAVLYWLCIMKYSRSYQILLFNRVCKGWYRWSTARVEE	120
QY	121	IIFGANMKMSWPKLLIHRFYLLKKQKMRPIGANYESRMTSKALTDLVYSITEKRS	180
DB	121	IIFGANMKMSWPKLLIHRFYLLKKQKMRPIGANYESRMTSKALTDLVYSITEKRS	180

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OM protein - protein search, using sw model

Run on: July 11, 2006, 08:26:26 ; Search time 192 Seconds
(without alignments)
1254.964 Million cell updates/sec

Title: US-10-765-456-1

Sequence: 1 MNQISKNDLSLDVLQDEWQK.....YWEIMQFHNKROQLRAIIE 527

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

1: A_Geneseqp_8: *
2: geneseqp1980s: *
3: geneseqp1990s: *
4: geneseqp2000s: *
5: geneseqp2001s: *
6: geneseqp2002s: *
7: geneseqp2003as: *
8: geneseqp2003bs: *
9: geneseqp2004s: *
10: geneseqp2005s: *
10: geneseqp2006s: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2790	100.0	527	8	ADRI4865 F. oxyspor
2	2550	91.4	527	8	ADRI4866 F. oxyspor
3	227.5	8.2	439	5	ABP26156 Streptococ
4	212.5	7.6	420	6	ADBO6930 Alloiococ
5	212.5	7.6	420	6	ADBO6930 Alloiococ
6	212.5	7.6	420	6	ADBO6930 Alloiococ
7	212.5	7.6	420	6	ADBO6930 Alloiococ
8	212.5	7.6	420	6	ADBO6930 Alloiococ
9	212.5	7.6	420	6	ADBO6930 Alloiococ
10	212.5	7.6	420	6	ADBO6930 Alloiococ
11	212.5	7.6	420	6	ADBO6930 Alloiococ
12	212.5	7.6	420	6	ADBO6930 Alloiococ
13	212.5	7.6	420	6	ADBO6930 Alloiococ
14	212.5	7.6	420	6	ADBO6930 Alloiococ
15	212.5	7.6	420	6	ADBO6930 Alloiococ
16	212.5	7.6	420	6	ADBO6930 Alloiococ
17	210.5	7.5	431	6	ADBO6930 Alloiococ
18	210.5	7.5	431	6	ADBO6930 Alloiococ
19	207.5	7.4	449	6	ADBO6930 Alloiococ
20	194	7.0	425	5	ABP28457 Streptococ
21	194	6.9	435	9	ABP28457 Streptococ
22	192	6.8	395	9	ABP28457 Streptococ
23	189.5	6.8	628	9	ADVI16529 E. faecal

24	185	6.6	420	9	AED01445
25	185	6.6	455	9	AED01451
26	180	6.5	506	6	ABU33605
27	178.5	6.4	599	2	AAW63835
28	178.5	6.4	599	2	AAW61974
29	178.5	6.4	599	2	AAW29984
30	178.5	6.4	599	3	AAW58019
31	172	6.2	496	7	ABO64657
32	171	6.1	638	7	ADG94292
33	168.5	6.0	605	7	ABO72234
34	162	5.8	479	6	ABW70135
35	153.5	5.5	449	9	AED01457
36	148.5	5.3	824	4	ABG10260
37	148	5.3	565	7	ABO68712
38	147	5.3	3207	4	ABG10131
39	146	5.2	574	7	ABO68655
40	145	5.2	1426	4	ABG11978
41	142.5	5.1	913	4	ABG02186
42	142.5	5.1	913	4	ABG14899
43	141.5	5.1	1144	4	ABG33203
44	140.5	5.0	832	8	ADH22665
45	138	4.9	514	4	ABG04464

ALIGNMENTS

RESULT 1
ADRI4865
ID ADRI4865 standard; protein; 527 AA.

AC ADRI4865;

DT 04-NOV-2004 (first entry)

DE F. oxysporum reverse transcriptase from pFOX2.

KW Reverse transcriptase; RT; pFOX2; pFOX3; 3' mismatch; cDNA synthesis;

KW small RNA; small interfering RNA; RNA interference; gene silencing;

KW siRNA.

OS Fusarium oxysporum.

XX US2004157213-A1.

PD 12-AUG-2004.

PF 26-JAN-2004; 2004US-00765456.

PR 27-JAN-2003; 2003US-0442885P.

PR 02-APR-2003; 2003US-0459775P.

PA (KENN/) KENNEDY J C.

PI Kennell JC;

DR WPI: 2004-580263/56.

DR N-PSDB: ADRI4867, ADRI4869.

PT New isolated fungal reverse transcriptases with enhanced capabilities,

PT and encoding nucleic acid molecules, useful for research and diagnostic

PT applications.

PS Claim 1; SEQ ID NO 1; 35pp; English.

XX The invention relates to an isolated polynucleotide comprising a sequence
XX that encodes a reverse transcriptase polypeptide or a fragment of a
XX reverse transcriptase polypeptide comprising a sequence having 88%
XX identity to ADRI4865 or ADRI4866, the reverse transcriptases encoded by
XX Fusarium oxysporum plasmids pFOX2 and pFOX3. Also included are
XX recombinant vector comprising a polynucleotide sequence (encoding the
XX reverse transcriptases) appearing as ADRI4867-ADRI4870, a cell comprising
XX an isolated polynucleotide that encodes a pFOX-RT, making a pFOX-RT

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OM protein - protein search, using sw model

Run on: July 11, 2006, 08:36:01 ; Search time 605 Seconds
(without alignments)
1330.092 Million cell updates/sec

Title: US-10-765-456-1
Perfect score: 2790
Sequence: 1 MNQISKSDSDVUDQEMGQK.....YWEIMQPHNLRKQQLRAIE 527

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 8366291 seqs, 1526956180 residues

Total number of hits satisfying chosen parameters: 8366291

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

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1: Pending Patents AA Main:*
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40: /EMC_Celerra_SIDS3/prodata/2/paa/US110_COMB.pep.*
41: /EMC_Celerra_SIDS3/prodata/2/paa/US111_COMB.pep.*
42: /EMC_Celerra_SIDS3/prodata/2/paa/US112_COMB.pep.*
43: /EMC_Celerra_SIDS3/prodata/2/paa/US113_COMB.pep.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2790	100.0	527	37 US-10-765-456-1	Sequence 1, App1
2	2550	91.4	527	37 US-10-765-456-2	Sequence 2, App1
3	227.5	8.2	439	34 US-10-415-182A-1488	Sequence 1488, Ap
4	212.5	7.6	420	1 PCT-US02-36123-312	Sequence 312, App
5	212.5	7.6	420	1 PCT-US02-36123-564	Sequence 564, App
6	212.5	7.6	420	1 PCT-US02-36123-870	Sequence 870, App
7	212.5	7.6	420	1 PCT-US02-36123-4116	Sequence 4116, Ap
8	212.5	7.6	420	1 PCT-US02-36123-6084	Sequence 6084, Ap
9	212.5	7.6	420	35 US-10-501-282-312	Sequence 312, App
10	212.5	7.6	420	35 US-10-501-282-564	Sequence 564, App
11	212.5	7.6	420	35 US-10-501-282-870	Sequence 870, App
12	212.5	7.6	420	35 US-10-501-282-4116	Sequence 4116, Ap
13	212.5	7.6	420	35 US-10-501-282-6084	Sequence 6084, Ap
14	212.5	7.6	431	1 PCT-US02-36123-314	Sequence 314, App
15	212.5	7.6	431	1 PCT-US02-36123-566	Sequence 566, App
16	212.5	7.6	431	1 PCT-US02-36123-872	Sequence 872, App
17	212.5	7.6	431	1 PCT-US02-36123-1598	Sequence 1598, Ap
18	212.5	7.6	431	1 PCT-US02-36123-3944	Sequence 3944, Ap
19	212.5	7.6	431	1 PCT-US02-36123-3952	Sequence 3952, Ap
20	212.5	7.6	431	1 PCT-US02-36123-4118	Sequence 4118, Ap
21	212.5	7.6	431	1 PCT-US02-36123-6086	Sequence 6086, Ap
22	212.5	7.6	431	35 US-10-501-282-314	Sequence 314, App
23	212.5	7.6	431	35 US-10-501-282-566	Sequence 566, App
24	212.5	7.6	431	35 US-10-501-282-872	Sequence 872, App
25	212.5	7.6	431	35 US-10-501-282-1598	Sequence 1598, Ap
26	212.5	7.6	431	35 US-10-501-282-3944	Sequence 3944, Ap
27	212.5	7.6	431	35 US-10-501-282-3952	Sequence 3952, Ap
28	212.5	7.6	431	35 US-10-501-282-4118	Sequence 4118, Ap
29	212.5	7.6	431	35 US-10-501-282-6086	Sequence 6086, Ap
30	210.5	7.5	420	1 PCT-US02-36123-858	Sequence 858, App
31	210.5	7.5	420	35 US-10-501-282-858	Sequence 858, App
32	210.5	7.5	431	1 PCT-US02-36123-860	Sequence 860, App
33	210.5	7.5	431	35 US-10-501-282-860	Sequence 860, App
34	194	7.0	425	34 US-10-415-182A-9910	Sequence 9910, Ap
35	194	7.0	436	34 US-10-415-182A-6090	Sequence 6090, Ap
36	190.5	6.8	467	22 US-09-252-691-6535	Sequence 6535, Ap
37	190.5	6.8	467	22 US-09-252-691-6535	Sequence 6535, Ap
38	190.5	6.8	467	34 US-10-417-986-6535	Sequence 6535, Ap
39	189.5	6.7	528	35 US-10-558-119-224	Sequence 224, App
40	187.5	6.6	529	1 PCT-US99-004049-6	Sequence 6, App1
41	185.5	6.6	529	30 US-10-008-618-6	Sequence 6, App1
42	185	6.6	420	37 US-10-797-262-2	Sequence 2, App1
43	185	6.6	455	37 US-10-797-262-8	Sequence 8, App1
44	180	6.5	506	1 PCT-US07-091078-61529	Sequence 61529, A
45	180	6.5	506	32 US-10-282-122A-61529	Sequence 61529, A

ALIGNMENTS

RESULT 1
US-10-765-456-1
; Sequence 1, Application US/10765456
; GENERAL INFORMATION:

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OW nucleic - nucleic search, using sw model

Run on: July 11, 2006, 06:46:21 ; Search time 8843 Seconds
(without alignment)
11454.565 Million cell updates/sec

Title: US-10-765-456-3
Perfect score: 1584
Sequence: 1 atgagcaacatcctcaaaa.....tcaggcgctataatgagtag 1584

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 6366136 seqs, 31973710525 residues
Total number of hits satisfying chosen parameters: 12732272

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

GenBml:*

1: gb env:*
2: gb_pat:*
3: gb_ph:*
4: gb_pl:*
5: gb_pr:*
6: gb_ro:*
7: gb_scs:*
8: gb_sy:*
9: gb_un:*
10: gb_vl:*
11: gb_ov:*
12: gb_hcg:*
13: gb_in:*
14: gb_om:*
15: gb_da:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1564.8	98.8	1905	4	AF124843 Fusarium
2	1563.2	97.4	1726	4	AF005241 Fusarium
3	1185.6	74.8	1836	4	AF124844 Fusarium
4	68.2	4.3	7218	2	166494 Sequence 14
5	64.4	4.1	785	4	AF005240 Fusarium
6	50.8	3.2	2000	2	AX655393 Sequence
7	48.4	3.1	14461	2	AX256438 Sequence
8	48.2	3.0	2000	2	AX655393 Sequence
9	46.2	2.9	335050	13	PFA293356 Plasmid
10	45.8	2.9	104492	12	AC023358 Homo sapi
11	45.8	2.9	157097	12	AC027784 Homo sapi
12	45.8	2.9	184864	5	AC018927 Homo sapi
13	45.4	2.9	2000	2	AX508575 Sequence
14	45.4	2.9	84723	4	AC010675 Arabidops
15	45.4	2.9	114505	4	P20P5 AC002062 Sequence
16	44.8	2.8	147079	5	AL772262 Human DNA
17	44.6	2.8	2822	5	AB169417 Macaca fa
18	44	2.8	164834	6	AL929043 Mouse DNA

c	19	44	2.8	209762	6	AC114822	AC114822 Mus muscu
c	20	43.8	2.8	194562	12	AC174219	AC174219 Bos tauru
c	21	43.8	2.8	266757	12	AC152522	AC152522 Bos tauru
c	22	43.6	2.8	157485	12	AC079056	AC079056 Homo sapi
c	23	43.6	2.8	179929	5	AC006270	AC006270 Homo sapi
c	24	43.6	2.8	181716	12	AC068285	AC068285 Homo sapi
c	25	43.4	2.7	212412	12	AC173526	AC173526 Bos tauru
c	26	43.2	2.7	100953	5	AC009489	AC009489 Homo sapi
c	27	43.2	2.7	115863	5	HSJ537P22	AL109733 Human DNA
c	28	43.2	2.7	163604	12	AC181686	AC181686 Strongylo
c	29	43.2	2.7	192972	5	CNS07EP9	AL512360 Human chr
c	30	43.2	2.7	306749	12	AL590310	AL590310 Homo sapi
c	31	42.8	2.7	73565	5	AC067962	AC067962 Homo sapi
c	32	42.8	2.7	171849	12	AC175179	AC175179 Bos tauru
c	33	42.8	2.7	213849	12	AC149749	AC149749 Bos tauru
c	34	42.8	2.7	249292	12	AC151082	AC151082 Bos tauru
c	35	42.6	2.7	171718	12	AC022501	AC022501 Homo sapi
c	36	42.6	2.7	175069	12	AC164693	AC164693 Bos tauru
c	37	42.4	2.7	156794	12	CT027830	CT027830 Danio rer
c	38	42.4	2.7	173690	11	EX465211	EX465211 Zebrafish
c	39	42.4	2.7	202612	12	CR848046	CR848046 Danio rer
c	40	42.2	2.7	160455	5	AL161897	AL161897 Human DNA
c	41	42.2	2.7	161593	5	HSBA49G10	AL121901 Human DNA
c	42	42.2	2.7	174413	12	AC011788	AC011788 Homo sapi
c	43	42.2	2.7	192120	12	AC163486	AC163486 Mus muscu
c	44	42.2	2.7	208992	6	AC153881	AC153881 Mus muscu
c	45	42.2	2.7	211591	12	AC160717	AC160717 Bos tauru

ALIGNMENTS

RESULT 1
AF124843
LOCUS
DEFINITION
Fusarium oxysporum f. sp. raphani mitochondrial plasmid pFOX2, complete sequence.
ACCESSION
AF124843
VERSION
AF124843.1 GI:5052323
KEYWORDS
ORGANISM
Fusarium oxysporum f. sp. raphani
SOURCE
mitochondrion Fusarium oxysporum f. sp. raphani
REFERENCE
1 (bases 1 to 1905)
Waltner,T.C. and Kennell,J.C.
Linear mitochondrial plasmid of F. oxysporum are novel,
telomere-like retrorselements
Mol. Cell 4 (2), 229-238 (1999)
JOURNAL
PUBMED
10488338
REFERENCE
2 (bases 1 to 1905)
Kennell,J.C. and Waltner,T.C.
Direct Submission
JOURNAL
Submitted (30-JAN-1999) Biological Sciences, Southern Methodist
University, 220 Foundren Science, Dallas, TX 75275-0376, USA
FEATURES
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1. 1905
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272.._1855
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OM nucleic - nucleic search, using sw model

Run on: July 11, 2006, 06:46:35 ; Search time 7954 Seconds
(without alignments)
11136.060 Million cell updates/sec

Title: US-10-765-456-3
Perfect score: 1584
Sequence: 1 atgacatcaatccctaaataa.....tcagggctataatcagtag 1584

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 48236798 seqs, 27959665780 residues

Total number of hits satisfying chosen parameters: 96473596

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :
EST:
1: gb_esc1:*
2: gb_esc3:*
3: gb_esc4:*
4: gb_esc5:*
5: gb_esc6:*
6: gb_esc7:*
7: gb_esc8:*
8: gb_esc9:*
9: gb_esc10:*
10: gb_esc11:*
11: gb_esc12:*
12: gb_esc13:*
13: gb_esc14:*
14: gb_esc15:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	87.6	5.5	281	10	DM177370 DM59 Fusa
2	57.6	3.6	997	14	CNS005TE AL060767 Drosophi
3	50.8	3.2	1687	1	AM090701 AM090701
4	50.4	3.2	1101	14	CNS00396 AL063921 Drosophi
5	48.8	3.1	1101	14	CNS012VN AL102077 Drosophi
6	47.2	3.0	1050	14	AG133232 Pan trogl
7	47.2	3.0	1101	14	CNS0006J AL062049 Drosophi
8	47	3.0	956	14	CT070073 Sus scro
9	47	3.0	1007	14	CNS000JOV AL076752 Drosophi
10	46	2.9	1101	14	CNS0106X AL098595 Drosophi
11	45.8	2.9	828	14	CNS011TX AL100719 Drosophi
12	45.4	2.9	1101	14	CNS000D1 AL065414 Drosophi
13	44.8	2.8	684	14	BZ433974 BOM0576TF
14	44.8	2.8	777	11	BZ071235 lK956407
15	44.8	2.8	786	11	BH938760 cdd13b10
16	44.8	2.8	1342	10	DV781885 Hw_Fat_17
17	44.4	2.8	742	14	AG469000 Mus muscu
18	44.4	2.8	839	14	DU959126 Drosophi
19	44.4	2.8	1204	14	CNS016E2 AL106628 Drosophi

C 20	44	2.8	616	14	CNS006L2	AL065735 Drosophi
C 21	43.8	2.8	657	13	CZ926091	CZ926091 109842112
C 22	43.8	2.8	756	13	DU270450	DU270450 109838000
C 23	43.8	2.8	888	14	CNS02C98	AL130853 Tetradon
C 24	43.8	2.8	1474	12	CG749456	CG749456 P043-3-CO
C 25	43.2	2.7	501	12	CG965772	CG965772 BO1F18TR
C 26	43.2	2.7	605	11	BH704585	BH704585 BOHVD15TR
C 27	43.2	2.7	653	11	BH855525	BH855525 BOMEA53TF
C 28	43.2	2.7	667	11	BH533961	BH533961 BOCIG69TF
C 29	43.2	2.7	667	11	BH538544	BH538544 BOH1T68TR
C 30	43.2	2.7	683	11	BH992999	BH992999 oeh28912
C 31	43.2	2.7	691	11	BH946440	BH946440 ODU88B10
C 32	43.2	2.7	697	11	BH961943	BH961943 odd97B09
C 33	43.2	2.7	704	11	BZ055027	BZ055027 jnr31B06
C 34	43.2	2.7	721	11	BH972815	BH972815 ood62d10
C 35	43.2	2.7	731	11	BH714645	BH714645 BOMHW93TF
C 36	43.2	2.7	740	11	BZ060417	BZ060417 11998603
C 37	43.2	2.7	753	11	BZ089251	BZ089251 1K267d10
C 38	43.2	2.7	756	11	BH688650	BH688650 BOMFW96TR
C 39	43.2	2.7	760	11	BH421764	BH421764 BOHNV79TF
C 40	43.2	2.7	760	12	CC943672	CC943672 BOIC880TR
C 41	43.2	2.7	822	11	BH655342	BH655342 BOMIR43TF
C 42	43.2	2.7	825	11	BH501985	BH501985 BOCGC94TR
C 43	43.2	2.7	840	11	BH498276	BH498276 BOMWA29TF
C 44	43.2	2.7	1005	11	BZ468099	BZ468099 BOMKO65TR
C 45	43.2	2.7	1054	11	BZ504662	BZ504662 BONIJ13TR

ALIGNMENTS

RESULT 1	DM177370	281 bp	mRNA	linear	EST 29-DEC-2005
LOCUS	DM177370				
DEFINITION	DM177370				
ACCESSION	DM177370				
VERSION	DM177370.1				
KEYWORDS	EST				
SOURCE	Fusarium culmorum				
ORGANISM	Fusarium culmorum				
REFERENCE	Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium.				
AUTHORS	Lysoe E., Bone K. and Klemsdal S.				
TITLE	Differential Display RT-PCR in high zearelenone producing strains				
JOURNAL	Unpublished (2005)				
COMMENT	Contact: Lysoe E Bioforsk Plantehelset Genetics and biotechnology Høgskoleveien 7, 1432 Aas, Norway Tel: +47 69949252 Fax: +47 64947110 Email: erik.lysoe@bioforsk.no				
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	/db_xref="taxon:5516"				
	/clone_lib="Fusarium culmorum Differential Display library"				
ORIGIN					
Query Match	5.5%; Score 87.6; DB 10; Length 281;				
Best Local Similarity	57.2%; Pred. No. 4.1e-12;				
Matches 159; Conservative	0; Mismatches 119; Indels 0; Gaps 0;				
Qy	151	GAATGATTAAGAGAGCAAGCAAAATGATATCTTCCTCCAGGCAAGG	210		
Db	2	GGAATTAAGTACTCTGACGACAGCAAGCAAAATGATATCTTAATTTCCAGGAGATGACA	61		
Qy	211	ATTGTTAGCGCAATAGAACCGCGCAATTCTGTAAGCACTGCTAGTGGCTATGTTTA	270		

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OM nucleic - nucleic search, using sw model

Run on: July 11, 2006, 06:49:55 ; Search time 1662 Seconds
(without alignments)
10453.069 Million cell updates/sec

Title: US-10-765-456-3

Perfect score: 1584
Sequence: 1 atgaatcaaatctctcaaaaa.....tcaggcctcaatcgagtag 1584

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 18892170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters: 37784340

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA Main:4

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3: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09_PUBCOMB.seq:*
4: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
5: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
6: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10_PUBCOMB.seq:*
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8: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1584	100.0	1584	8	US-10-765-456-3 Sequence 3, Appli
2	1564.8	96.8	1905	8	US-10-765-456-5 Sequence 4, Appli
3	1204.8	76.1	1584	8	US-10-765-456-4 Sequence 4, Appli
4	1185.6	74.8	1836	8	US-10-765-456-6 Sequence 6, Appli
5	45.4	2.9	2000	3	US-09-938-842A-3270 Sequence 3270, Ap
6	45.4	2.9	2000	3	US-09-938-842A-3270 Sequence 3270, Ap
7	42.8	2.7	1330	10	US-10-956-157-281 Sequence 281, App
8	42.8	2.7	1330	10	US-10-956-157-281 Sequence 281, App
9	42.2	2.7	660	6	US-10-123-155-480 Sequence 480, App
10	42.2	2.7	660	7	US-10-146-731-480 Sequence 480, App
11	42.2	2.7	660	7	US-10-140-472-480 Sequence 480, App
12	42.2	2.7	660	7	US-10-141-761-480 Sequence 480, App
13	42.2	2.7	660	7	US-10-142-885-480 Sequence 480, App
14	42.2	2.7	660	7	US-10-158-790-480 Sequence 480, App
15	42.2	2.7	660	7	US-10-137-871-480 Sequence 480, App
16	42.2	2.7	660	7	US-10-140-923-480 Sequence 480, App
17	42.2	2.7	660	7	US-10-141-756-480 Sequence 480, App

18	42.2	2.7	660	7	US-10-141-759-480	Sequence 480, App
19	42.2	2.7	660	7	US-10-140-805-480	Sequence 480, App
20	42.2	2.7	660	7	US-10-140-864-480	Sequence 480, App
21	41.4	2.6	5798	7	US-10-311-455-1639	Sequence 1639, App
22	40.2	2.5	476	4	US-09-925-065A-278144	Sequence 278144, App
23	40.2	2.5	476	5	US-09-925-065A-278144	Sequence 278144, App
24	40.2	2.5	485	12	US-10-301-480-355166	Sequence 355166, App
25	40.2	2.5	485	12	US-10-301-480-368575	Sequence 368575, App
26	39.8	2.5	616	4	US-09-925-065A-767274	Sequence 767274, App
27	39.8	2.5	616	5	US-09-925-065A-767274	Sequence 767274, App
28	39.8	2.5	2064	8	US-10-282-122A-16800	Sequence 16800, App
29	39.6	2.5	639	8	US-10-424-599-99767	Sequence 99767, App
30	39.6	2.5	10395	8	US-10-323-281-782	Sequence 782, App
31	39.4	2.5	3673778	7	US-10-312-841-1	Sequence 1, Appli
32	39	2.5	2133	10	US-10-750-185-27952	Sequence 27952, A
33	39	2.5	2133	10	US-10-750-623-27952	Sequence 27952, A
34	38.8	2.4	616	4	US-09-925-065A-767275	Sequence 767275, A
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45	38.4	2.4	621	7	US-10-027-632-220659	Sequence 220659, A

ALIGNMENTS

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US-10-765-456-3
Sequence 3, Application US//10765456
Publication No. US20040157213A1
GENERAL INFORMATION:
APPLICANT: Kennell, John C.
TITLE OF INVENTION: Fungal Reverse Transcriptases with Enhanced Capabilities
FILE REFERENCE: SL002-010
CURRENT FILING DATE: 2004-01-26
PRIOR APPLICATION NUMBER: 60/442,885
PRIOR FILING DATE: 2003-01-27
NUMBER OF SEQ ID NOS: 39
SOFTWARE: Microsoft Word 2000
SEQ ID NO 3
LENGTH: 1584
TYPE: DNA
ORGANISM: fungal
US-10-765-456-3
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 1584; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 61 AAGACCTTGAGTCAGAAAGAAATCTTGTGATGAGGATTAATCTTCAATCGCTAGG 120
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DB 121 AGTATAGTAGTATCCCATTTTTCGAGAGGAATTAATACGAGATCAAGAAAGCA 180
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DB 181 AATAGATATCTTCCCTTCAGAGAGCAAGATTTGATCGCAATAGAAACCGCGAAATT 240
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GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on: July 11, 2006, 06:47:12 ; Search time 320 Seconds

(without alignments)
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Title: US-10-765-456-3

Perfect score: 1584
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Gapop 10.0 , Gapext 1.0

Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 2807332

Minimum DB seq length: 0
Maximum DB seq length: 2000000000Post-processing: Minimum Match 0*
Maximum Match 100*

Listing first 45 summaries

Database :

Issued Patents NA:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	39.6	2.5	818128	3	US-09-949-016-14547
5	39.6	2.5	818128	3	US-09-949-016-14548
6	39.6	2.5	818128	3	US-09-949-016-14549
7	39.6	2.5	818128	3	US-09-949-016-14550
8	39.6	2.5	818128	3	US-09-949-016-14551
9	39.6	2.5	818128	3	US-09-949-016-14552
10	39.6	2.5	818128	3	US-09-949-016-14553
11	39.6	2.5	818128	3	US-09-949-016-14554
12	39.6	2.5	818128	3	US-09-949-016-14555
13	39.6	2.5	818128	3	US-09-949-016-14556
14	39.6	2.5	818128	3	US-09-949-016-14557
15	39.6	2.5	818128	3	US-09-949-016-14558
16	39.6	2.5	818128	3	US-09-949-016-14559
17	39.6	2.5	818128	3	US-09-949-016-14560
18	39.6	2.5	818128	3	US-09-949-016-14561
19	39.6	2.5	818128	3	US-09-949-016-14562
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22	39.6	2.5	818128	3	US-09-949-016-14565
23	39.6	2.5	818128	3	US-09-949-016-14566

C 24	38.4	2.4	194537	3	US-09-949-016-12928	Sequence 12928, A
C 25	38.4	2.4	201529	3	US-09-949-016-12740	Sequence 12740, A
C 26	38.2	2.4	1141	3	US-09-806-708B-22	Sequence 22, Appl
C 27	37.8	2.4	3540	3	US-02-452-136-5	Sequence 5, Appl
C 28	37.8	2.4	19503	3	US-09-949-016-16528	Sequence 16528, A
C 29	37.6	2.4	94095	3	US-09-949-016-14369	Sequence 14369, A
C 30	37.6	2.4	237863	3	US-09-949-016-13404	Sequence 13404, A
C 31	37.2	2.3	601	3	US-09-949-016-12752	Sequence 12752, A
C 32	37.2	2.3	601	3	US-09-949-016-12851	Sequence 12851, A
C 33	37.2	2.3	601	3	US-09-949-016-10709	Sequence 50769, A
C 34	37.2	2.3	601	3	US-09-949-016-50768	Sequence 50768, A
C 35	37.2	2.3	77851	3	US-09-949-016-12508	Sequence 12508, A
C 36	37.2	2.3	77867	3	US-09-949-016-13211	Sequence 13211, A
C 37	37.2	2.3	77867	3	US-09-949-016-13212	Sequence 13212, A
C 38	37.2	2.3	77940	3	US-09-949-016-12509	Sequence 12509, A
C 39	37.2	2.3	211049	3	US-09-949-016-15770	Sequence 15770, A
C 40	36.8	2.3	1395	3	US-09-248-796A-5435	Sequence 5435, Ap
C 41	36.8	2.3	5032	3	US-09-566-921-14	Sequence 14, Appl
C 42	36.8	2.3	21136	3	US-09-949-016-13748	Sequence 13748, A
C 43	36.8	2.3	69813	3	US-09-949-016-12455	Sequence 12455, A
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C 45	36.8	2.3	69813	3	US-09-949-016-13906	Sequence 13906, A

ALIGNMENTS

RESULT 1
US-08-232-463-14/c
Sequence 14, Application US/08232463
Patent No. 5670367
GENERAL INFORMATION:
APPLICANT: DORNER, F.
APPLICANT: SCHERFLINGER, F.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
FILING DATE:
APPLICATION NUMBER: EP 91 114 300.6
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET INFORMATION: 30472/114 IMMU
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
TELEFAX: (703)683-4109
TELEX: 899149
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE: